

Supplementary Table 1 – Difference in gene expression between WTC and non WTC cases - FDR ≤ 0.1 and |FCH|≥1.5

Genes (down-reg)	Log <sub>2</sub> (WTC vs. non-WTC)	WTC vs. non-WTC	FDR	Genes (up-reg)	Log <sub>2</sub> (WTC vs. non-WTC)	WTC vs. non-WTC	FDR	Genes (up-reg)	Log <sub>2</sub> (WTC vs. non-WTC)	WTC vs. non-WTC	FDR
BCL6	-0.94	-1.92	0.0415	AMB P	1.3	2.46	0.0632	IL4	1.5	2.83	0.0546
C1S	-0.93	-1.91	0.0117	BAGE	1.65	3.15	0.0316	IL9	1.22	2.33	0.0282
CD163	-1.2	-2.3	0.0477	BIRC5	1.16	2.24	0.0444	IRF3	1.08	2.11	0.0006
CD53	-0.86	-1.82	0.0994	C4B	2.14	4.42	0.0251	KIR3DL3	1.6	3.02	0.0415
CD58	-0.75	-1.69	0.0188	C6	1.63	3.09	0.0219	KIR_Activating_Subgroup_1	0.79	1.72	0.0662
CEBPB	-1.05	-2.08	0.0172	C8G	1.41	2.66	0.0172	LILRA1	1.22	2.33	0.0373
CSF1	-1.12	-2.17	0.0033	CCL16	0.93	1.9	0.0253	LTK	0.94	1.91	0.0444
CTSH	-0.91	-1.88	0.0079	CCL26	1.05	2.07	0.0493	MAGEC2	1.36	2.56	0.0726
CTSL	-0.62	-1.54	0.0089	CCR9	0.86	1.81	0.0807	MASP2	1.95	3.86	0.0089
CX3CL1	-1.18	-2.27	0.0118	CD1A	1.34	2.53	0.0180	MIF	0.95	1.93	0.0057
CXCL10	-2.14	-4.4	0.0128	CD24	1.3	2.46	0.0070	MNX1	1.93	3.81	0.0509
CXCL12	-1.03	-2.05	0.0206	CD3EAP	1.11	2.16	0.0064	MPPED1	1.2	2.3	0.0509
ETS1	-0.91	-1.88	0.0138	CD70	1.11	2.16	0.0628	OSM	1.84	3.59	0.0160
GZMB	-1.14	-2.21	0.0715	CD79B	1.26	2.4	0.0570	PASD1	1.42	2.67	0.0330
HLA-DPB1	-0.97	-1.95	0.0415	CFI	0.81	1.75	0.0697	PBK	1.03	2.04	0.0330
HLA-DRA	-1.13	-2.19	0.0391	CR2	1.75	3.37	0.0089	PLA2G1B	1.25	2.38	0.0615
HLA-G	-1.44	-2.72	0.0097	CREBBP	0.84	1.8	0.0182	PLA2G6	0.78	1.72	0.0070
HMGB1	-0.62	-1.53	0.0032	CTCFL	1.29	2.44	0.0633	S100A7	1.67	3.18	0.0273
IFI16	-0.65	-1.57	0.0608	CX3CR1	1.21	2.32	0.0415	SPACA3	0.99	1.99	0.0712
IFITM1	-1.22	-2.33	0.0096	CXCR1	0.99	1.99	0.0684	SPINK5	2.02	4.07	0.0168
IL13RA2	-1.07	-2.09	0.0444	EBI3	0.96	1.94	0.0456	SPO11	1.19	2.29	0.0693
ITGA5	-1.33	-2.52	0.0160	ELANE	1.23	2.34	0.0615	TCF7	0.82	1.77	0.0562
LGALS3	-1.21	-2.31	0.0128	ENTPD1	0.84	1.8	0.0398	TFE3	0.63	1.54	0.0742
MAPK1	-0.82	-1.76	0.0006	FADD	1.16	2.23	0.0012	TFEB	0.8	1.74	0.0070
MRC1	-1.14	-2.2	0.0078	ICAM4	0.87	1.82	0.0743	TIRAP	0.65	1.57	0.0078
MSR1	-0.97	-1.96	0.0493	IFNA7	1.47	2.76	0.0493	TLR9	0.92	1.89	0.0493

<b>NFATC2</b>	-1.55	-2.92	0.0012	<b>IFNB1</b>	1.1	2.15	0.0415	<b>TNFRSF11B</b>	1.28	2.42	0.0171
<b>PDGFRB</b>	-0.72	-1.65	0.0182	<b>IFNG</b>	1.41	2.65	0.0415	<b>TNFSF11</b>	1.43	2.69	0.0373
<b>STAT5B</b>	-0.82	-1.77	0.0170	<b>IFNL1</b>	1.92	3.77	0.0015	<b>TNFSF13</b>	1.61	3.05	0.0003
<b>TFRC</b>	-0.76	-1.7	0.0353	<b>IGLL1</b>	1.48	2.8	0.0391	<b>TNFSF15</b>	1.16	2.23	0.0072
<b>TGFB2</b>	-0.87	-1.82	0.0591	<b>IL12A</b>	1.42	2.67	0.0247	<b>TPTE</b>	1.22	2.33	0.0605
<b>UBC</b>	-0.78	-1.72	0.0570	<b>IL12RB1</b>	1.5	2.84	0.0198	<b>TRAF2</b>	0.81	1.75	0.0006
<b>VCAM1</b>	-0.76	-1.69	0.0585	<b>IL13</b>	1.36	2.57	0.0391	<b>ULBP2</b>	1.34	2.52	0.0245
<b>YTHDF2</b>	-0.67	-1.6	0.0180	<b>IL17F</b>	1.15	2.23	0.0376	<b>ZNF205</b>	1.01	2.01	0.0006
<b>NOL7</b>	-0.7	-1.62	0.0078	<b>IL19</b>	1.02	2.02	0.0608	<b>CC2D1B</b>	1.44	2.72	0.0012
<b>USP39</b>	-0.73	-1.65	0.0165	<b>IL22RA2</b>	1.27	2.4	0.0788	<b>GPATCH3</b>	0.9	1.86	0.0168
				<b>IL23A</b>	1.1	2.14	0.0570	<b>GUSB</b>	0.65	1.57	0.0206
				<b>IL24</b>	1.6	3.03	0.0330	<b>PPIA</b>	0.84	1.79	0.0024
				<b>IL25</b>	1.02	2.03	0.0391	<b>SF3A3</b>	0.84	1.79	0.0020
				<b>IL26</b>	1.44	2.71	0.0477				
				<b>IL2RB</b>	0.94	1.92	0.0596				
				<b>IL3</b>	1.35	2.55	0.0591				

Supplementary Table 2: Genes in the Hallmark pathway collection

Hallmark Collection	Genes in Set
Protein Secretion	ARCN1, TMED10, COPB2, RAB14, ATP7A, COPB1, LAMP2, EGFR, IGF2R, COPE, PPT1, AP3S1, BET1, CLCN3, AP2S1, CLTC, AP2M1, RER1, KIF1B, ARF1, OCRL, ICA1, MON2, ARFGEF2, TMED2, NAPG, TMX1, PAM, SCAMP1, SH3GL2, RAB2A, COG2, VAMP3, ERGIC3, DOPEY1, VAMP4, VPS4B, NAPA, GNAS, STX7, SEC22B, VPS45, STX16, YKT6, SNX2, ARFGEF1, CLTA, CLN5, M6PR, SGMS1, USO1, TSG101, DNM1L, LMAN1, YIPF6, ARFIP1, ANP32E, TSPAN8, DST, SCRNI, SEC31A, VAMP7, SCAMP3, AP2B1, RAB22A, AP3B1, TPD52, ATP6V1H, GBF1, KRT18, CAV2, ATP1A1, BNIP3, ZW10, GALC, ADAM10, RAB5A, GOLGA4, SEC24D, AP1G1, MAPK1, GOSR2, RPS6KA3, STAM, ABCA1, SNAP23, SOD1, GLA, ATP6V1B1, STX12, CD63, TOM1L1, SSPN, ARFGAP3, RAB9A, CTSC
DNA Repair	POLR2H, POLR2A, POLR2G, POLR2E, POLR2J, POLR2F, POLR2C, POLR2K, GTF2H3, POLR2D, ERCC3, DDB2, POLR1C, XPC, PCNA, POLR2I, SUPT4H1, POLD3, POLR3GL, POLR3C, GTF2B, POLR1D, NCBP2, RDBP, GTF2F1, ERCC5, LIG1, ERCC1, ERCC4, POLD4, COBRA1, RFC2, ELL, TAF10, RRM2B, SUPT5H, RPA3, SNAPC5, SSRP1, RFC3, RPA2, TCEB3, TAF12, TH1L, TAF13, TAF6, TAF9, GTF2A2, VPS37D, NME1, RNMT, ERCC2, POLE4, VPS37B, NT5C3, SNAPC4, AAAS, ZNRD1, RFC4, ITPA, POM121, BRF2, RFC5, SAC3D1, CLP1, NME4, PRIM1, VPS28, TSG101, USP11, TAF1C, TARBP2, POLH, CETN2, POLD1, CANT1, PDE4B, DGCR8, RAD51, SURF1, PNP, ADA, NME3, GTF3C5, NT5C, AK1, GTF2H1, HCLS1, APRT, ERCC8, IMPDH2, POLB, SDCBP, SF3A3, DAD1, UPF3B, GUK1, TP53, ADRM1, SEC61A1, POLA2, FEN1, ZNF707, NUDT9, PDE6G, TYMS, BCAP31, DDB1, NFX1, RAD52, ADCY6, ARL6IP1, DGUOK, POLL, SMAD5, MPG, DUT, POLA1, EIF2C4, RALA, ZWINT, BCAM, TK2, CSTF3, GTF2H5, HPRT1, BOLA2, GPX4, BRP44, CDA, THOC4, MRPL40, NPR2, REV3L, EDF1, DFNA5, TMED2, STX3, RAE1, UMPS, EIF1B, AK3, NUDT21, RBX1, SRSF6, GMPR2, DCTN4, COX17, CMPK2, CCNO
G2M Checkpoint	AURKA, CCNA2, TOP2A, CCNB2, CENPA, BIRC5, CDC20, PLK1, TTK, PRC1, NDC80, KIF11, NUSAP1, CKS2, KIF2C, MKI67, AURKB, TPX2, SMC4, BUB1, CENPF, RACGAP1, CENPE, KIF23, UBE2C, MCM6, MCM3, PTTG1, CDK1, KIF4A, ESPL1, MAD2L1, NEK2, KIF22, HMMR, KPNA2, CDKN3, CDC25A, H2AFX, CDC25B, PLK4, CDC6, CCNF, MCM5, LMNB1, E2F3, KIF15, CHEK1, UBE2S, WHSC1, HMGB3, DBF4, TACC3, MCM2, CDKN2C, CDKN1B, FANCC, NASP, STAG1, GINS2, FBXO5, POLQ, EZH2, RAD21, STMN1, SUV39H1,

	PRIM2, E2F1, CHAF1A, NOLC1, GSPT1, BUB3, SMC1A, ILF3, CDC7, INCENP, CKS1B, EXO1, H2AFZ, TFDP1, CCND1, KPNB1, HN1, LBR, HUS1, KIF20B, TOP1, PDS5B, SRSF1, STIL, ABL1, DTYMK, CDC27, BARD1, ATF5, CDC45, ODC1, XPO1, SFPQ, TMPO, PML, BRCA2, CTCF, CASC5, SETD8, SLC38A1, TRA2B, MYBL2, TROAP, PAPD7, CUL3, MAPK14, HIST1H2BK, MYC, AMD1, CBX1, CHMP1A, DKC1, YTHDC1, CCNT1, TGFB1, ATRX, LIG3, NUP50, SLC7A5, RBL1, NUMA1, RAD54L, EFNA5, PRPF4B, UCK2, ARID4A, CUL1, UPF1, DR1, MNAT1, SMC2, RBM14, RPA2, SQLE, ORC6, CDK4, POLE, RASAL2, HOXC10, RPS6KA5, CUL4A, SLC7A1, FOXN3, HMGA1, SS18, TRAIP, PRMT5, CUL5, DDX39A, MARCKS, PBK, ORC5, SAP30, KATNA1, HNRNPD, POLA2, HIRA, HIF1A, SYNCRI, TLE3, NCL, RAD23B, E2F2, EGF, HMGN2, SRSF10, SNRPD1, CASP8AP2, SMARCC1, SLC12A2, NOTCH2, TNPO2, SMAD3, ZAK, HSPA8, G3BP1, PTTG3P, DMD, MEIS1, HNRNPU, SRSF2, MT2A, NUP98, EWSR1, KIF5B, MTF2, E2F4, BCL3, PURA, MEIS2, PAFAH1B1, WRN, H2AFV, ODF2
Glycolysis	PGK1, ALDOA, ENO1, TPI1, PFKP, ERO1L, ALDOB, VEGFA, MXI1, PKM2, HK2, LDHA, EXT1, SLC25A10, GUSB, PFKFB1, PGAM1, PYGB, AK4, P4HA1, PMM2, FAM162A, SDC1, EGLN3, PC, B4GALT7, FBP2, IGFBP3, CHPF, B3GAT3, CHST12, HS2ST1, MPI, GNPDA1, AKR1A1, PPFIA4, B3GAT1, CHPF2, G6PD, MDH2, CHST6, PGLS, PGAM2, CHST1, GPC1, TSTA3, ALG1, GFPT1, PRPS1, GOT1, MDH1, SLC35A3, GALK1, EGFR, ANGPTL4, CITED2, PLOD2, QSOX1, ME2, SPAG4, P4HA2, GAPDHS, ENO2, GOT2, EXT2, SLC25A13, HMMR, PDK3, CXCR4, GPC4, ECD, GNE, B4GALT2, FUT8, MIOX, VCAN, GPC3, B3GALT6, HSPA5, ME1, ADORA2B, UGP2, MIF, NANP, ZNF292, STC2, TPST1, PGM2, GYS1, TKTL1, TGFA, CHST2, PHKA2, STMN1, GALE, MET, LCT, IRS2, POLR3K, B4GALT1, EFNA3, LHX9, KDELR3, TALDO1, DPYSL4, VLDLR, CD44, AGL, SOX9, DDT4, IDUA, CASP6, GLCE, COPB2, DSC2, HS6ST2, CDK1, PLOD1, SDC2, GMPPB, PAXIP1, NSDHL, RARS, SLC16A3, GLRX, SRD5A3, SDC3, HDLBP, COL5A1, CLDN9, TFF3, STC1, KIF20A, GYS2, SLC37A4, LHPP, SDHC, NASP, AURKA, B3GNT3, ISG20, LDHC, ARPP19, CENPA, HOMER1, BIK, CYB5A, HAX1, COG2, IL13RA1, NOL3, CLDN3, AGRN, CLN6, TXN, PAM, CAPN5, PKP2, ABCB6, DCN, GMPPA, BPNT1, ANG, GPR87, GAL3ST1, ALDH7A1, NT5E, IDH1, PYGL, NDUFV3, NDST3, PPP2CB, PSMC4, TPBG, TGFBI, GALK2, CTH, KIF2A, CACNA1H, ANKZF1, SAP30, RBCK1, ELF3, RPE, B4GALT4, DEPDC1, RRAGD, IER3, ALDH9A1, DLD, MERTK, GCLC, FKBP4, SOD1, MED24, AK3, XYLT2, ARTN, PPIA, CHST4

Supplemental Table 3. Testing differences in overall Pathway activity: GSVA Hallmark (batch)(FDR<0.1)

	IgFCH_WvC	FCH_WvC	pvals_WvC	fdrs_WvC	StatusFC H1FDR0. 1_WvC
HALLMARK_DNA_REPAIR	1.48	2.79	0.00385	0.094	1
HALLMARK_G2M_CHECKPOINT	2.05	4.15	0.00768	0.094	1
HALLMARK_PROTEIN_SECRETION	-1.33	-2.51	0.0073	0.094	-1
HALLMARK_GLYCOLYSIS	1.82	3.52	0.0055	0.094	1

Supplementary Table 4: Testing differences in overall Pathway activity: GSVA Cell type (batch)(FDR<0.1)

	IgFCH_W vC	FCH_W vC	pvals_W vC	fdrs_W vC	StatusFC H1FDR0.1 WvC	geneInPTW
NK CD56bright cell	2.08	4.23	0.000707	0.017	1	FOXJ1,MPPED1,PLA2G6, RRAD,,,
NK cell	2.13	4.39	0.002997	0.036	1	BCL2,FUT5,NCR1,ZNF205 ,,,
Th17 cell	1.52	2.88	0.008122	0.065	1	IL17A,IL17RA,RORC,,,

Supplemental Table 5. Pathway analysis in rat prostate RNA-seq (WTC vs. normal air)

pathway	t
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT ( 108 )	17.21
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_ ( 72 )	14.11
KEGG_OXIDATIVE_PHOSPHORYLATION ( 104 )	13.21
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT ( 57 )	11.81
KEGG_PEROXISOME ( 73 )	10.47

KEGG_PARKINSONS_DISEASE ( 100 )	9.60
REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS ( 420 )	9.59
MIPS_PA700_20S_PA28_COMPLEX ( 36 )	7.88
REACTOME_FATTY_ACID_TRIACYLGLYCEROL_AND_KETONE_BODY_METABOLISM ( 154 )	7.80
KEGG_HUNTINGTONS_DISEASE ( 146 )	7.58
KEGG_CITRATE_CYCLE_TCA_CYCLE ( 30 )	7.50
BIOCARTA_PROTEASOME_PATHWAY ( 28 )	7.44
MIPS_26S_PROTEASOME ( 22 )	7.33
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION ( 38 )	7.25
REACTOME_CDT1_ASSOCIATION_WITH_THE_CDC6_ORC_ORIGIN_COMPLEX ( 54 )	7.00
REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX ( 62 )	6.84
REACTOME_REGULATION_OF_ORNITHINE_DECARBOXYLASE_ODC ( 48 )	6.22
REACTOME_M_G1_TRANSITION ( 76 )	5.95
KEGG_PROTEASOME ( 44 )	5.86
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES ( 179 )	5.73
REACTOME_ORC1_REMOVAL_FROM_CHROMATIN ( 65 )	5.52
KEGG_FATTY_ACID_METABOLISM ( 35 )	5.45
REACTOME_SIGNALING_BY_WNT ( 58 )	5.45
REACTOME_SYNTHESIS_OF_DNA ( 89 )	5.45
REACTOME_ER_PHAGOSOME_PATHWAY ( 53 )	5.43
REACTOME_S_PHASE ( 104 )	5.43
REACTOME_CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES ( 45 )	5.42
REACTOME_MITOTIC_G1_G1_S_PHASES ( 123 )	5.39
REACTOME_VIF_MEDIATED_DEGRADATION_OF_APOBEC3G ( 48 )	5.37

REACTOME_CDK_MEDIATED_PHOSPHORYLATION_AND_REMOVAL_OF_CDC6 ( 46 )	5.33
REACTOME_AUTODEGRADATION_OF_THE_E3_UBIQUITIN_LIGASE_COP1 ( 47 )	5.31
REACTOME_TRIGLYCERIDE BIOSYNTHESIS ( 37 )	5.30
REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITEADIPOCYTE_DIFFERENTIATION ( 66 )	5.24
REACTOME_P53_DEPENDENT_G1_DNA_DAMAGE_RESPONSE ( 53 )	5.20
REACTOME_CHOLESTEROL BIOSYNTHESIS ( 20 )	5.20
REACTOME_G1_S_TRANSITION ( 104 )	5.07
REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_EMI1 ( 49 )	4.98
REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APCC ( 55 )	4.97
REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE ( 40 )	4.86
REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT ( 41 )	4.78
MIPS_PA700_COMPLEX ( 20 )	4.71
MIPS_55S_RIBOSOME_MITOCHONDRIAL ( 71 )	4.54
KEGG_STEROID BIOSYNTHESIS ( 15 )	4.49
MIPS_20S_PROTEASOME ( 14 )	4.43
REACTOME_P53_INDEPENDENT_G1_S_DNA_DAMAGE_CHECKPOINT ( 48 )	4.41
REACTOME_SCFSKP2_MEDIATED_DEGRADATION_OF_P27_P21 ( 53 )	4.35
REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECECTOR_BCR ( 87 )	4.31
REACTOME_CITRIC_ACID_CYCLE_TCA_CYCLE ( 19 )	4.30
REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION_ ( 61 )	4.25
REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION ( 64 )	4.23
REACTOME_CELL_CYCLE_CHECKPOINTS ( 108 )	4.23
REACTOME_MITOCHONDRIAL_FATTY_ACID_BETA_OXIDATION ( 12 )	4.19
REACTOME_HIV_INFECTON ( 172 )	4.19

REACTOME_ACTIVATION_OF_NF_KAPPAB_IN_B_CELLS ( 57 )	4.06
REACTOME_REGULATION_OF_APOPTOSIS ( 55 )	4.04
REACTOME_DESTABILIZATION_OF_MRNA_BY_AUF1_HNRNP_D0 ( 49 )	4.03
MIPS_PA28_20S_PROTEASOME ( 16 )	4.02
REACTOME_METABOLISM_OF_VITAMINS_AND_COFACTORS ( 46 )	3.98
KEGG_PYRUVATE_METABOLISM ( 36 )	3.96
REACTOME_GENERIC_TRANSCRIPTION_PATHWAY ( 123 )	3.95
REACTOME_FATTY_ACYL_COA BIOSYNTHESIS ( 18 )	3.90
REACTOME_AP_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS ( 64 )	3.81
REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION ( 181 )	3.70
REACTOME_BRANCHED_CHAIN_AMINO_ACID_CATABOLISM ( 16 )	3.63
REACTOME_VITAMIN_B5_PANTOTHENATE_METABOLISM ( 10 )	3.58
KEGG_LYSINE_DEGRADATION ( 39 )	3.58
KEGG_STEROID_HORMONE BIOSYNTHESIS ( 36 )	3.36
REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS ( 46 )	3.34
KEGG_BUTANOATE_METABOLISM ( 32 )	3.27
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450 ( 43 )	3.23
REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION ( 210 )	3.19
REACTOME_NUCLEOTIDE_EXCISION_REPAIR ( 41 )	3.15
KEGG_PPAR_SIGNALING_PATHWAY ( 62 )	3.11
REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELEMENTS ( 78 )	3.10
REACTOME_AP_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_AP_C_CDH1_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1 ( 63 )	3.08
KEGG_ALZHEIMERS_DISEASE ( 142 )	3.08

REACTOME_NUCLEAR_RECECTOR_TRANSCRIPTION_PATHWAY ( 41 )	3.01
KEGG_GNRH_SIGNALING_PATHWAY ( 88 )	-3.00
KEGG_TYPE_I_DIABETES_MELLITUS ( 20 )	-3.01
MIPS_H2AX_COMPLEX_ISOLATED_FROM_CELLS_WITHOUT_IR_EXPOSURE ( 12 )	-3.08
REACTOME_NEUROTRANSMITTER_RECECTOR_BINDING_AND_DOWNSTREAM_TRANSMISSION_IN_THE_POSTSYNAPTIC_CELL ( 128 )	-3.09
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION ( 59 )	-3.11
REACTOME_COLLAGEN_FORMATION ( 37 )	-3.13
REACTOME_NCAM_SIGNALING_FOR_NEURITE_OUT_GROWTH ( 56 )	-3.14
PID_CD8TCRDOWNSTREAMPATHWAY ( 49 )	-3.15
BIOCARTA_AGR_PATHWAY ( 32 )	-3.15
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_ANDEIFS_AND_SUBSEQUENT_BINDING_TO_43S ( 51 )	-3.23
REACTOME_RNA_POL_I_PROMOTER_OPENING ( 14 )	-3.24
BIOCARTA_ACH_PATHWAY ( 15 )	-3.29
REACTOME_PACKAGING_OF_TELOMERE_ENDS ( 17 )	-3.30
PID_AVB3_INTEGRIN_PATHWAY ( 61 )	-3.30
REACTOME_PHOSPHOLIPASE_C_MEDIANDED_CASCADE ( 48 )	-3.31
REACTOME_ACETYLCHOLINE_NEUROTRANSMITTER_RELEASE_CYCLE ( 10 )	-3.40
REACTOME_ACTIVATION_OF_NMDA_RECECTOR_UPON GLUTAMATE_BINDING_AND_POSTSYNAPTIC_EVENTS ( 36 )	-3.54
KEGG_PATHWAYS_IN_CANCER ( 290 )	-3.64
REACTOME_POTASSIUM_CHANNELS ( 93 )	-3.75
REACTOME_AMYLOIDS ( 24 )	-3.79
PID_IL12_STAT4PATHWAY ( 28 )	-3.81

KEGG_CALCIUM_SIGNALING_PATHWAY ( 164 )	-3.82
REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX ( 44 )	-3.86
PID_FGF_PATHWAY ( 49 )	-3.87
KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM ( 74 )	-3.91
KEGG_ECM_RECECTOR_INTERACTION ( 65 )	-4.01
PID_SYNDECAN_4_PATHWAY ( 29 )	-4.01
KEGG_DILATED_CARDIOMYOPATHY ( 79 )	-4.02
REACTOME_GLYCOSAMINOGLYCAN_METABOLISM ( 92 )	-4.11
REACTOME_STRIATED_MUSCLE_CONTRACTION ( 26 )	-4.19
REACTOME_SMOOTH_MUSCLE_CONTRACTION ( 22 )	-4.22
BIOCARTA_STATHMIN_PATHWAY ( 18 )	-4.51
MIPS_TRBP_CONTAINING_COMPLEX_1 ( 23 )	-4.83
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS ( 55 )	-5.03
KEGG_FOCAL_ADHESION ( 175 )	-5.32
REACTOME_NCAM1_INTERACTIONS ( 32 )	-5.42
KEGG_CELL_ADHESION_MOLECULES_CAMS ( 103 )	-5.43
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC ( 63 )	-5.50
PID_SYNDECAN_1_PATHWAY ( 37 )	-5.52
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SYNAPSES ( 174 )	-5.58
MIPS_40S_RIBOSOMAL_SUBUNIT_CYTOPLASMIC ( 29 )	-5.80
REACTOME_MUSCLE_CONTRACTION ( 44 )	-6.07
REACTOME_TRANSLATION ( 135 )	-6.45
REACTOME_NEURONAL_SYSTEM ( 261 )	-7.24
REACTOME_INFLUENZA_LIFE_CYCLE ( 118 )	-7.50

REACTOME_AXON_GUIDANCE ( 213 )	-7.78
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE ( 100 )	-8.92
MIPS_60S_RIBOSOMAL_SUBUNIT_CYTOPLASMIC ( 45 )	-9.48
REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION ( 88 )	-10.91
MIPS_NOP56P_ASSOCIATED_PRE_RRNA_COMPLEX ( 95 )	-10.91
REACTOME_NONSENSE_MEDIANED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX ( 94 )	-11.37
REACTOME_3_UTR_MEDIANED_TRANSLATIONAL_REGULATION ( 96 )	-11.71
KEGG_RIBOSOME ( 80 )	-14.22
MIPS_RIBOSOME_CYTOPLASMIC ( 76 )	-14.24
REACTOME_PEPTIDE_CHAIN_ELONGATION ( 78 )	-15.33